

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1.-22. (Canceled)

23. (New) A method for identifying at least one endogenous molecule that differs in abundance between a first cell population and a second cell population, comprising:

(a) comparing a first Fourier Transform Mass Spectrometry (FTMS) peak profile obtained from the first cell population with a second FTMS peak profile obtained from the second cell population, wherein the first peak profile and the second peak are obtained independently;

(b) identifying at least one peak that differs in intensity in the first FTMS peak profile relative to the second FTMS peak profile, which said at least one peak corresponds to least one molecule that differs in abundance between a first cell population and a second cell population; and

(c) identifying said at least one molecule that differs in abundance between the first cell population and the second cell population either directly from mass-to-charge (m/z) ratio of said at least one peak or through additional fragmentation of said at least one molecule;

thereby identifying at least one molecules that differ in abundance between a first cell population and a second cell population.

24. (New) A method for identifying at least one endogenous molecule that differs in abundance between a first cell population and a second cell population, comprising:

(a) comparing a first FTMS peak profile obtained from the first cell population with a second FTMS peak profile obtained from the second cell population, wherein the first peak profile and the second peak profile are not obtained concurrently and wherein the first and second cell populations do not contain a label;

(b) identifying at least one peak that differs in intensity in the first FTMS peak profile relative to the second FTMS peak profile, which said at least one peak corresponds to least one molecule that differs in abundance between a first cell population and a second cell population; and

(c) identifying said at least one molecule that differs in abundance between the first cell population and the second cell population either directly from mass-to-charge

(m/z) ratio of said at least one peak or through additional fragmentation of said at least one molecule;

thereby identifying at least one molecules that differ in abundance between a first cell population and a second cell population.

25. (New) A method for identifying at least one endogenous molecule that differs in abundance between a first cell population and a second cell population, comprising:

(a) comparing a first FTMS peak profile obtained from the first cell population with a second FTMS peak profile obtained from the second cell population, wherein the first peak profile and the second peak profile are obtained from whole cell extracts;

(b) identifying at least one peak that differs in intensity in the first FTMS peak profile relative to the second FTMS peak profile, which said at least one peak corresponds to least one molecule that differs in abundance between a first cell population and a second cell population; and

(c) identifying said at least one molecule that differs in abundance between the first cell population and the second cell population either directly from mass-to-charge (m/z) ratio of said at least one peak or through additional fragmentation of said at least one molecule;

thereby identifying at least one molecules that differ in abundance between a first cell population and a second cell population.

26. (New) The method of claim 25, wherein the whole cell extract is a solvent-extracted cell extract.

27. (New) The method of claim 25, wherein the whole cell extract is desalted.

28. (New) The method of any one of claims 23 to 27, further comprising:

(c) prior to step (a), obtaining the first FTMS peak profile from the first cell population by subjecting said first cell population to FTMS.

29. (New) The method of any one of claims 23 to 27, further comprising:

(c) prior to step (a), obtaining the second FTMS peak profile from the second cell population by subjecting said second cell population to FTMS.

30. (New) The method of claim 28, further comprising:

(d) prior to step (a), obtaining the second FTMS peak profile from the second cell population by subjecting said second cell population to FTMS.

31. (New) The method of any one of claims 23 to 27, wherein the first cell population is a reference cell population and the second cell population is a test cell population.

32. (New) The method of claim 31, wherein the first and second cell population are of different cell types.

33. (New) The method of claim 32, wherein the first and second cell populations are of different tissue types from the same organism.

34. (New) The method of claim 32, wherein the first and second cell populations are of the same tissue type from different organisms.

35. (New) The method of any one of claims 23 to 27, wherein the first and second cell populations are of the same cell type.

36. (New) The method of claim 35, wherein the first cell population is a normal cell population and the second cell population is a diseased cell population and wherein the at least one molecule is a marker of the disease.

37. (New) The method of claim 36, wherein the diseased cell population is a cancerous cell population and wherein the marker is a marker for cancer.

38. (New) The method of claim 37, wherein the cancerous cell population is a population of melanoma, myeloid leukemia, or carcinoma cells.

39. (New) The method of claim 38, wherein the carcinoma is lung, breast, ovarian, colon, kidney, prostate, pancreatic, stomach, brain, lymphatic system, thymic, thyroid, adrenal or testicular carcinoma.

40. (New) The method of claim 36, wherein the diseased cell population is from an individual with cardiovascular disease and wherein the marker is a marker for cardiovascular disease.

41. (New) The method of claim 40, wherein the diseased cell population is a population of cardiomyocytes, endothelial cells, macrophages, hepatocytes, adipocytes, smooth muscle cells or intestinal cells.

42. (New) The method of claim 36, wherein the diseased cell population is from an individual with diabetes.

43. (New) The method of claim 42, wherein the diseased cell population is a population of cardiomyocytes, endothelial cells, macrophages, pancreatic cells, hepatocytes, adipocytes, smooth muscle cells or intestinal cells.

44. (New) The method of claim 36, wherein the diseased cell population is from an obese individual.

45. (New) The method of claim 44, wherein the diseased cell population is a population of cardiomyocytes, endothelial cells, macrophages, hepatocytes, adipocytes, smooth muscle cells or intestinal cells.

46. (New) The method of claim 35, wherein the first cell population has not been subjected to a test agent and the second cell population has been subjected to the test agent.

47. (New) The method of claim 46, wherein the test agent is a known drug.

48. (New) The method of claim 46, wherein the test agent is a drug candidate.

49. (New) The method of claim 46, wherein the test agent is a small molecule.

50. (New) The method of claim 46, wherein the test agent is a protein.

51. (New) The method of claim 50, wherein the protein is a hormone, a growth factor, a cytokine, a ligand, or an antibody.

52. (New) The method of claim 46, wherein the test agent is a nucleic acid.

53. (New) The method of claim 52, wherein the nucleic acid is an antisense nucleic acid, a triple helix nucleic acid, or a ribozyme.

54. (New) The method of claim 46, wherein the nucleic acid is a DNA, an RNA, or a DNA-RNA hybrid.

55. (New) The method of claim 31, wherein the first FTMS peak profile is a historical control.

56. (New) The method of claim 31, wherein the first FTMS peak profile is a concurrent control.

57. (New) The method of any one of claims 23 to 27, wherein the first and second cell populations are populations of primary cells from a tissue or organ.

58. (New) The method of claim 5747, wherein in the primary cells are primary brain, skin, lung, endothelial, epithelial, adipose, muscle, bone, stomach, colon, spleen, pancreas, kidney, bladder, heart, lymphatic system, blood, or liver cells.